AUTHOR INDEX

to Volume 141, September–December 1995

Alberghina, L., 903
Albertson, D. G., 527
Albinder, B., 1399
Alleman, M., 347, 361
Ambroziak, J., 1425
Anderson, J. A., 721
Andrews, J. D., 587
Anxolabéhère, D., 1407
Aquadro, C. F., 413
Arndt, K. T., 857
Ashfield, T., 1597
Atchley, W. R., 1189
Atkinson, M., 721
Atlan, A., 1015
Auerbach, C., 1
Avery, L., 1365
Aviv, D. H., 813
Ayala, F. J., 1225

Bae, E., 191
Bähler, J., 61
Baker, N. E., 607
Bandelt, H.-J., 743
Banks, G. K., 1225
Barbash, D. A., 1451
Barnes, T. M., 159
Barry, E. G., 909
Beck, C. F., 937
Bedian, V., 595
Bennetzen, J. L., 373
Bernard, M., 721
Bhargava, J., 75
Bilder, D., 1087
Bjerke, M., 1061
Blackman, R. K., 271
Blouin, M. S., 1007
Bolshakov, V. N., 1075
Boore, J. L., 305
Bopp, D., 1521
Bossie, C. A., 271
Boutis, P., 1351
Bregliano, J.-C., 571, 579
Brickner, J., 1315
Brody, M. S., 15
Brown, W. M., 305
Bríza, J., 383
Butcher, D., 431
Butler, D. K., 909
Buzzell, R. I., 1597

Cacheiro, N. L. A., 1547
Capowski, E. E., 1383
Cardenas, M. E., 833
Carroll, B. J., 383
Castaño, I. B., 465
Castilloux, A.-M., 733
Chan, C. S., 1439
Chandler, V. L., 709
Chao, J.-L., 1075
Charlesworth, B., 1619
Charlesworth, D., 1619
Chin, G. M., 619
Chiu, Y.-H., 453
Christensen, A. C., 1037
Christman, M. F., 465
Churchill, G. A., 413
Cline, T. W., 1451
Coe, E. H., Jr., 709
Coen, D., 1407
Cohan, F. M., 1231
Colot, V., 1299
Cone, K. C., 709
Costantini, F., 321
Coulson, A., 159
Courtney, C. H., 1007
Crease, T. J., 1327
Culiat, C. T., 1563

Dame, J. B., 1007
Darlow, J. M., 825
Darvasi, A., 1199
De Couet, H. G., 1049
Degroote, F., 571
Delattre, M., 1407
Deminoff, S. J., 1263
Dillin, A., 889
Dinman, J. D., 95
Doebley, J., 333
Dolinski, K., 833
Dorer, D. R., 1037
Dorman, J. B., 1399
Doseff, A. I., 857
Dullum, C. J., 1537
Dunman, P. M., 813
Duricka, D., 283
Dutcher, S. K., 945

Eggleston, W. B., 347, 361
Ehler, L. L., 945
Elston, R. C., 1651
Engebrecht, J., 49
Eshed, Y., 1147
Ezekiel, D. H., 1037

Faris, J. D., 721
Fath, M. J., 25
Fernando, R. L., 1651
Ferris, P. J., 543
Feulner, G., 15
Finelli, A. L., 271
Fletcher, J. C., 1025
Fondrk, M. K., 1537
Fong, K. S. K., 1049
Fontdevila, A., 181
Forster, P., 743
Foss, M., 889
Freeman, K., 1253
Freeman, M. E., 629
Fujitani, Y., 797

Ganetzky, B., 203
Gelber, M. B., 551
Geyer, P. K., 191, 1061
Giasson, L., 491
Gloeckner, G., 937
Gloor, G. B., 587
Goodman, M. M., 1573
Green, M. M., 1075
Greenwald, I., 513
Grimes, C. D., 1425
Gustus, C., 333
Gwadz, M., 1253

Haack, K. R., 1245
Hackett, D. A., 1425
Hall, J. L., 87
Hankins, G. R., 629
Hawley, R. S., 619
Healy, M. J., 215
Heath-Pagliuso, S., 465
Hedgecock, E. M., 989
Heitman, J., 833
Hekimi, S., 159, 1351
Helfand, S. L., 1043
Hemenway, C. S., 833
Herman, R. K., 989
Hill, C. W., 15
Hill, K. K., 595
Hiller, M. A., 833
Hilliker, A. J., 263
Hodgkin, J., 527
Hoffmann, F. M., 595
Hollick, J. B., 709
Holmes, J. A., 945
Horabin, J. I., 1521
Hu, X., 607
Huang, G. S., 845
Huang, K. N., 1275
Hudson, R. R., 1605

Hughes, J., 147
Hulbert, S. H., 373
Humayun, M. Z., 813
Hunt, G. J., 1537
Huvos, P., 925

Infante, A., 87
Innes, R. W., 1597
Inomata, N., 237

Jacques, M., 1015
Jaw, T. J., 1075
Johnson, D. K., 1547, 1563
Johnson, E. A., 1061
Johnson, S. L., 1583
Jones, D. A., 383
Jones, E. W., 833
Jones, J. D. G., 383
Juang, J.-L., 595
Judd, B. H., 245
Judelson, H. S., 503

Kalderon, D., 1507
Kaplan, N. L., 1605
Karpen, G. H., 283
Keen, N. T., 1597
Keil, R. L., 845
Kenyon, C., 1399
Kermicle, J. L., 347, 361
Kieff, F. S., 465
Kilpatrick, S. T., 1113
King, L. M., 255
Kinzy, T. G., 481
Kirby, D. A., 1483
Klimyuk, V. I., 383
Kobayashi, I., 797
Kohara, Y., 159
Kohli, J., 61
Kolter, R., 25
Kriticou, D., 1225
Kronstad, J. W., 491
Kullman, J., 629
Kumar, S., 1641
Kuspa, A., 147
Kwiatowski, J., 1225

Lakowski, B., 1351
Laurençon, A., 571, 579
Laurenson, P., 889
Le, M.-H., 283
Leach, D. R. F., 825
Lee, E.-C., 607
Lee, J. J., 321
Lee, R. Y. N., 1365
Leibowitz, A., 181
Leroy, P., 721
Lessard, S., 733
Lewis, E. B., 1227
Li, W., 1507
Lieberman, H. B., 107
Lin, Y.-R, 391
Linder, C. R., 1163
Lisbin, M. J., 1101
Lissemore, J. L., 551
Litwin, S., 667
Liu, J., 1473
Llorente, B., 1015
Lo, S., 87
Loidl, J., 49
Loo, S., 889
Loomis, W. F., 147
Lotti, M., 903
Lu, Y. H., 721
Lyman, D. F., 1491
Lynch, T. J., 1315

MacDonald, D. E., 263
Mackinnon, M. J., 755
Maduro, M., 977
Maghakian, D., 147
Mahanty, H. K., 25
Maine, E. M., 551
Matson, S. W., 443
Matteson, P. G., 667
McCabe, D., 1439
McKim, K. S., 619
McLaughlin, P. J., 1049
Meléndez, A., 1507
Mendonca, V. M., 443
Mercot, H., 1015
Merriman, P. J., 1425
Metzenberg, R. L., 119
Metzger, J., 33
Miklos, G. L. G., 1049
Molnar, M., 61
Montchamp-Moreau, C., 1015
Montgomery, C. L., 1547
Montgomery, C. S., 1563
Morgan, M. T., 1619
Morris, N. R., 453, 1287
Murphy, H. S., 813
Myers, R. S., 805

Nag, D. K., 75
Nagoshi, R. N., 191, 1061
Nakano, K. J., 1315
Nei, M., 1641
Nelson, J. C., 721
Nussbaum, R. L., 667

Oakeshott, J. G., 215
Oakey, R. J., 667
Odgers, W. A., 215
Okuyama, E., 237
Orias, E., 1315
Orive, M. E., 1173
Otto, S. P., 1173

Padgett, R. W., 271
Page, R. E., Jr., 1537
Palejwala, V. A., 813
Paterson, A. H., 391
Patterson, G. I., 709
Patton, J. S., 191
Paulsen, J. E., 1383
Pearlson, N. J., 629
Pentz, E. S., 629
Pereira, H. S., 263
Perkins, D. D., 909
Perry, W. L., III, 321
Pesole, G., 903
Peterson, P. A., 1135
Pilgrim, D., 977
Pirrotta, V., 1439
Pryor, T. J., 373

Qian, S., 1439
Quiao, L., 551

Rahman, M. S., 813
Raizen, D. M., 1365
Raju, N. B., 909
Rand, D. M., 1113
Randall, T. A., 119
Reiner, D. J., 961
Richards, M. B., 743
Richter, T. E., 373
Rieseberg, L. H., 1163
Rinchik, E. M., 1563
Rine, J., 889
Robinson, A. S., 1225
Rockmill, B., 49, 75
Rodesch, C., 191
Rodesch, C. K., 1061
Roeder, G. S., 49, 75
Rogina, B., 1043
Rose, A. M., 1339
Roseman, R. R., 1061
Rossi, J. M., 321
Rossignol, J.-L., 1299
Roth, J. R., 1245
Russell, L. B., 1547, 1563
Rzhetsky, A., 771

Saccone, C., 903
Sadoff, B. U., 465
Sadosky, A. B., 15
Samson, M.-L., 1101
Sandt, C. H., 15
Santangelo, G. M., 1263
Santos, M., 181

Schedl, P., 1521
Scherthan, H., 49, 75
Schertz, K. F., 391
Schultz, S. T., 1209
Scott, M. J., 1225
Scott, M. P., 1087
Seiler, G. J., 1163
Sekelsky, J. J., 619
Shattock, R. C., 503
Sherman, J. D., 683
Shibata, H., 223, 237
Shore, D., 873, 1253
Shroyer, T., 1399
Shu, P., 551
Simmons, M. J., 1425
Simonsen, K. T., 413
Sipiczki, M., 61
Skinner, P., 1425
Smardon, A., 551
Smith, G. R., 33
Smith, H. G., 657
Sokolowski, M. B., 263
Soller, M., 1199
Song, K., 1473
Sorrells, M. E., 721
Spielman, L. J., 503
Stack, S. M., 683
Stahl, F. W., 805, 439–442
Stahl, M. M., 805
Stall, R. E., 675
Stathakis, D. G., 629
Stec, A., 333
Stephan, W., 1483
Stricker, C., 1651
Strome, S., 1383
Stubbs, L. J., 1563
Stuber, C. W., 1573
Sun, Y. H., 1075
Sussel, L., 873
Sykes, B., 743
Symington, L. S., 1275

Tai, P. C., 25
Thackeray, J. R., 203
Therman, E., 799
Thomas, C. M., 383
Thomas, J. H., 961
Thummel, C. S., 1025
Tilghman, S. M., 321, 667
Tornow, J., 1263
Tsai, C.-J., 1075

Vallejos, C. E., 675
Van Deynze, A. E., 721
Vannier, D., 873
Vasicek, T. J., 321
Veuille, M., 255
Virgin, J. B., 33

Wang, G., 813
Wang, J. F., 675
Waterbury, J., 1521
Waters, E. R., 785
Weeds, A. G., 1049
Weinshenker, D., 961
Welker, D., 147
Weller, J. I., 755
Weston, J. A., 1583
Wettermark, K.-J., 657
White, K., 1101
Wickner, R. B., 95
Wilkinson, H. A., 513
Williams, C. G., 1573
Willins, D. A., 1287
Willis, J. H., 1209
Wolfner, M. F., 1473
Woolford, J. L., Jr., 481
Wright, T. R. F., 629

Xiang, X., 1287
Xie, T., 271
Xu, J., 137
Xu, S., 1189, 1657

Yamamoto, K., 797
Yamazaki, T., 223, 237
Yang, Z., 1641
Yedvobnick, B., 1491
Yeh, J.-Y., 1075
Yowell, C. A., 1007
Yu, C.-T., 1075
Yu, Z. H., 675

Zacharias, H., 7
Zamir, D., 1147
Zawadzski, P., 1231
Zeng, L., 321
Zera, A. J., 1125
Zetka, M.-C., 1339
Zhang, C., 1125
Zhang, L. H., 25
Zhang, T., 321
Zhao, S., 15
Zhu, J., 1633
Zhu, Y., 465

SUBJECT INDEX

to Volume 141, September–December 1995

Acetylcholine receptor, nicotinic, MC neurotransmission and pharyngeal excitation in *Caenorhabditis elegans*, 1365

Adaptive protein evolution, molecular evolution of *Amy* locus in *Drosophila melanogaster* species subgroup, 223

Additive effect, QTL additive effect, estimation in half-sib design using maximum likelihood methodology, 755

Adenosine triphosphatase, hydrogen (H^+-ATPase), vacuolar assembly in *vph6* mutants of *Saccharomyces cerevisiae*, 833

Advanced intercross lines, experimental population for fine mapping of QTL, 1199

Agaricus bisporus, inbreeding depression in, 137

Age/aging, regulation of gene expression in *Drosophila*, 1043

Alkylating agents, induction of UV modulation of mutagenesis distinct from *E. coli* SOS and adaptive responses, 813

Allele
- alleles of phosphatase gene *PTC1* and of a gene encoding a putative basic leucine zipper protein, extragenic suppressors of *Saccharomyces cerevisiae pkc1* mutation and, 1275
- allelic interactions heritably altering activity of metastable maize *pl* allele, 709
- increased expression of *Saccharomyces cerevisiae TEF1* bypasses lethality of *TEF5* null allele, 481
- *R-stippled*
  - molecular organization and germinal instability, 347
  - paramutagenicity, 361
- *scabrous* mutant alleles from *Drosophila melanogaster*, 607
- transgenic insertional allele at *Fused* locus, *Hc46* locus in mouse, 321
- *XO*-feminizing mutations in *C. elegans*, regulatory *tra* alleles, 527

Ambers, amber mutants of phage T4 (*Perspectives*), 439

Amino acid sequence, inference method of reconstructing ancestral sequences, 1641

α-Amylase
- evolutionary relationships and sequence variation of *Amy* variants in *Drosophila melanogaster*, 223
- molecular evolution of *Amy* locus in *Drosophila melanogaster* species subgroup, 223

Aneuploidy, *7, 18* translocation nondisjunction (mouse), 667

Apis mellifera, foraging behavior, major QTL affecting, 1537

Ascobolus immersus, spore color gene *b2*, modulating effect of methylation induced premeiotically (MIP), 1299

Aspergillus nidulans, nuclear migration mutations
- extragenic suppressors of *nudC3* mutation, 453
- suppression by *tubA* alpha tubulin mutation, 1287

Auerbach, Charlotte (*In Memoriam*), 1

Avirulence genes, soybean resistance genes specific for different *Pseudomonas syringae* avirulence genes, 1597

Bacillus subtilis, transformation, size and continuity of DNA segments integrated in, 1231

"Background selection" effect
- effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
- pattern of neutral molecular variation under background selection model, 1619

Bacterial spot, genomic location of genes controlling hypersensitive reaction to Doidge Dye in tomatoes, 675

Bacteriophage
- amber mutants of phage T4 (*Perspectives*), 439
- effects of trinucleotide repeats on palindrome inviability in *E. coli* suggest hairpin folding preferences *in vivo*, 825

Body size, heritability and selection on body size in natural population of *Drosophila buzzatii*, 181

Breeding, inbreeding depression
- in *Agaricus bisporus*, 137
- individual variation in, 1209

Caenorhabditis elegans
- germline proliferation and viability, *mes-3* and, 1383
- *glp-1*-mediated cell signalling in, enhancers of *glp-1*, 551
- lifespan, *age-1* and *daf-2* genes in, 1383
- *lin-12* expression patterns during *C. elegans* hermaphrodite development, 513
- maternal-effect viable mutants and morphological/behavioral defects, 1351
- meiotic pattern of crossing over, *rec-1* mutant and, 1339
- muscle excitation in, genes in, 961
- *ncl-1* as cell marker for mosaic analysis of *lin-37* and *dpy-1*, 989
- neuronal *unc-119* gene, 977
- pharyngeal excitation in, genes required for MC neurotransmission, 1365
- quantitative analysis of recombination rates and gene density across the whole genome, 159

XO-feminizing mutations, regulatory *tra* alleles and *X* chromosome duplication, 527
Calcineurin, cation homeostasis in *Saccharomyces cerevisiae*, 833
Candida spp., evolutionary origin of nonuniversal CUG^{SER} codon in, 743
Cation homeostasis, *Saccharomyces cerevisiae*, calcineurin in, 833
Cell cycle, checkpoint controls responsive to DNA damage/incomplete DNA replication, extragenic suppressors of *Schizosaccharomyces pombe rad9* mutations and, 107
Cell differentiation, chromosome behavior in cell differentiation (*Perspectives*), 799
Cell fate, *lin-12* expression patterns during *C. elegans* hermaphrodite development, 513
Cell growth, EF 1β deficiency suppressed by EF-1α in *Saccharomyces cerevisiae*, 481
Chlamydomonas reinhardtii
  genomic library, in yeast artificial chromosomes, 87
  mating type locus, *nic-7*, *ac-29*, and *thi-10* genes in, 543
  position of mitotic spindle apparatus in *bld2–1* mutant lacking basal bodies, 945
  sexual differentiation, genes involved in light control of, 937
Chromatin, structure, *M26* recombination hotspot activity in *Schizosaccharomyces pombe* and, 33
Chromosome(s)
  artificial, construction of *Chlamydomonas reinhardtii* genomic library in yeast artificial chromosomes, 87
  barriers to introgression in *Helianthus*, 1163
  chloroplasts, heterochromatin, and polytene chromosomes (*Perspectives*), 7
  chromosome behavior in cell differentiation (*Perspectives*), 799
  chromosome maps of *Dictyostelium discoideum*, 147
  effect of yeast *MER* gene on chromosome synapsis and meiotic recombination, 49
  heteroduplex DNA formation and homolog chromosome pairing in yeast meiotic mutants, 75
  molecular-marker linkage map of wheat homoeologous groups 4, 5, and 7, 721
  rec8 gene of *Schizosaccharomyces pombe* in structure, pairing, and segregation of meiotic chromosomes during meiosis, 61
Chromosome 4, T-DNA locus, distribution of unlinked transposed dissociation elements in tomato, 383
Chromosome 17, *He46* locus in mouse, 321
Chromosome abnormalities
  7, 18 translocation nondisjunction (mouse), 667
  chromosomal duplications in *Salmonella typhimurium*, recombination between IS*200* elements and, 1245
  chromosome rearrangements involving nucleolus organizer region in *Neurospora*, 909
Coalescent model of neutral evolution, 413
Colicin V, *E. coli* periplasmic colicin V, 25
Complementation analysis, mutations encompassing *pink-eyed dilution (p)* locus of mouse, 1547
Computer simulation, Muller's ratchet, epistasis and mutation effects, 431
Corrigendum, 797, 1225
Crossing over, meiotic pattern of crossing over in *Caenorhabditis elegans*, *rec-1* mutant and, 1339
CUG^{SER} codon, nonuniversal, evolutionary origin in *Candida* spp., 743
Cytoplasmic incompatibility, variability within Seychelles cytoplasmic incompatibility system in *Drosophila simulans*, 1015
Cytoskeleton, position of mitotic spindle apparatus in *Chlamydomonas reinhardtii bld2–1* mutant lacking basal bodies, 945

Daphnia pulex, nucleotide variation in ribosomal DNA intergenic spacer arrays, 1327
Developmental genetics, analysis of conditional genetic effects and conditional variance components, 1633
Dictyostelium discoideum, chromosome maps of, 147
Dissociation (Ds) elements, unlinked transposed *Ds*s in tomato, 383
DNA
  checkpoint controls responsive to DNA damage/incomplete DNA replication, extragenic suppressors of *Schizosaccharomyces pombe rad9* mutations and, 107
  developmental DNA rearrangements (deletion) within five species of the *Tetrahymena pyriformis* species complex, 925
  effects of trinucleotide repeats on palindrome inviability in *E. coli* suggest hairpin folding preferences *in vivo*, 825
  heteroduplex DNA formation and homolog chromosome pairing in yeast meiotic mutants, 75
  mitochondrial. *See* Mitochondrial DNA
  organization of DNA in centric heterochromatin in *Drosophila Dp1187* minichromosome, 283
  polymorphism. *See* Polymorphism
  ribosomal, nucleotide variation in rDNA intergenic spacer arrays of *Daphnia pulex*, 1327
  sequence of mitochondrial genome of *Lumbricus terrestris*, 305
  size and continuity of DNA segments integrated in *Bacillus subtilis* transformation, 1231
  species-specific and mating type-specific DNA regions adjacent to mating type idiomorphs in *Neurospora* spp., 119
DNA repair
  Drosophila melanogaster mei-9 gene, 619

inducible repair-recombination system in female germline of *Drosophila melanogaster*
differential sensitivity to gamma rays, 579
effect of inhibitors of DNA synthesis and gamma rays, 571
DNA replication, *Saccharomyces cerevisiae* mutants requiring DNA topoisomerase I (*trf*), 465
DNA synthesis, inhibitors, effect on inducible repair-recombination system in female germline of *Drosophila melanogaster*, 571
Dominance
QTL dominance effect, estimation in half-sib design using maximum likelihood methodology, 755
teosinte branched II and evolution of maize, 333
Drosophila buzzatii, heritability and selection on body size in natural population, 181
Drosophila melanogaster
autosomal component of sex determination signal of *Drosophila melanogaster*, 1451
departure from neutrality in a segment of *white* gene, 1483
Dopa decarboxylase gene cluster, genetic and molecular organization, 629
evolutionary relationships and sequence variation of *Amy* variants in, 223
eye development, *white*$^+$ gene detection of transcriptional silencer elements, 1075
genome, S elements in, 1425
gypsy-P element mutagenesis, 1061
inducible repair-recombination system in female germline
differential sensitivity to gamma rays, 579
effect of inhibitors of DNA synthesis and gamma rays, 571
larval foraging behavior, *Chaser (Csr)* gene and, 263
mei-9 encodes a homologue of yeast excision repair protein Rad1, 619
mitochondrial DNA hitchhiking, frequency shifts of mtDNA variants and nuclear genetic background, 1113
molecular and mutational analysis of *flightless-I*, 1049
molecular evolution of *Amy* locus in species subgroup, 223
nucleotide polymorphism in *Esterase 6* 5'promotor region, 215
ovo and *otu* function in oogenesis, 191
P element mobility, *KP* leucine zipper and, 587
position-effect variegation, mutations of *zeste* as recessive enhancers, 245
regulation of gene expression during aging, 1043
scabrous mutations, 607
Triplo-lethal locus, 1037
Drosophila pseudoobscura, polymorphism at *Est-5B* locus, 255
Drosophila simulans, variability within Seychelles cytoplasmic incompatibility system, 1015
Drosophila spp.
DC2, second *Drosophila* protein kinase A catalytic subunit gene, 1507
effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
fs(1)Ya protein in nuclear envelope during early embryonic development, 1473
genetic interactions between Abelson (Abl) tyrosine kinase and failed axon connections (fax), 595
genomic regions required for midgut morphogenesis, 1087
interaction of ecdysone-inducible *BR-C* and *E74* genes in regulation of target gene transcription and *Drosophila* metamorphosis, 1025
molecular structure of centric heterochromatin in *Drosophila Dp1187* minichromosome, 283
Notch receptor activity and *Hairless* function during adult external sensory organ development, 1491
P transposase-induced events on *P* transgene, prevalence of localized rearrangements *vs.* transpositions, 1407
selection and maintenance of sexual identity in *Drosophila* germline, 1521
suppressed nonsense mutations at *elav* locus, 1101
tolkin gene in development, 271
Ultrabithorax (Ubx) gene expression in imaginal tissues, parasegmental and imaginal disc enhancers and, 1439
Drosophila virilis, alternative splicing patterns and splicing signals in sodium channel gene *para*, 203

Ecdysone, interaction of ecdysone-inducible *BR-C* and *E74* genes in regulation of target gene transcription and *Drosophila* metamorphosis, 1025
Elongation factor(s), EF 1β deficiency suppressed by EF-1α in *Saccharomyces cerevisiae*, 481
Enhancer elements, *Drosophila Ultrabithorax (Ubx)* gene expression in imaginal tissues, parasegmental and imaginal disc enhancers and, 1439
Epistasis
Muller's ratchet, epistasis and mutation effects, 431
teosinte branched II and evolution of maize, 333
Escherichia coli
alkylating agent-induced UV modulation of mutagenesis distinct from SOS and adaptive responses, 813
colicin V secretion pathway, 25
decay of χ recombination hotspot activity in, 805
effects of trinucleotide repeats on palindrome inviability in *E. coli* suggest hairpin folding preferences *in vivo*, 825
Δ*helD* and Δ*uvrD* mutations in RecF recombination pathway in, 443
Rhys elements, 15

Esterase-5B enzyme activity, polymorphism at *Est-5B* locus in *Drosophila pseudoobscura* and, 255
Esterase 6 enzyme activity, polymorphism in *Est 6* 5'promotor region in *Drosophila melanogaster* and, 215
Eye development, *Drosophila melanogaster, white*$^{+}$ gene detection of transcriptional silencer elements, 1075

Fertility selection, Fundamental Theorem of Natural Selection in Ewens' sense, 733
Finite polygenic mixed model extended to linkage analysis, quantitative trait loci, 1651
Foraging behavior
Drosophila melanogaster larva, *Chaser (Csr)* gene and, 263
honey bee, major QTL affecting, 1537

Gametogenesis, *Chlamydomonas reinhardtii*, genes involved in light control of, 937
Gamma radiation, effect on inducible repair-recombination system in female germline of *Drosophila melanogaster*, 571, 579
Gene(s)
age-1 and *daf-2* genes in controlling lifespan of *Caenorhabditis elegans*, 1383
alleles of phosphatase gene *PTC1* and of a gene encoding a putative basic leucine zipper protein, extragenic suppressors of *Saccharomyces cerevisiae pkc1* mutation and, 1275
alternative splicing patterns and splicing signals in *Drosophila* sodium channel gene *para*, 203
Ascobolus immersus spore color gene *b2*, modulating effect of methylation induced premeiotically (MIP), 1299
barriers to introgression in *Helianthus*, 1163
Chaser (Csr) and larval foraging behavior in *Drosophila melanogaster*, 263
contribution of *deadpan (dpn)* to sex determination signal of *Drosophila melanogaster*, 1451
DC2, second *Drosophila* protein kinase A catalytic subunit gene, 1507
departure from neutrality in a segment of *white* gene of *Drosophila melanogaster*, 1483
Dopa decarboxylase gene cluster of *Drosophila melanogaster*, genetic and molecular organization, 629
Drosophila Ultrabithorax (Ubx) gene expression in imaginal tissues, parasegmental and imaginal disc enhancers and, 1439
effect of yeast *MER* gene on chromosome synapsis and meiotic recombination, 49
evolutionary relationships and sequence variation of *Amy* variants in *Drosophila melanogaster*, 223
extragenic suppressors of *nudC3* mutation in *Aspergillus nidulans*, 453
genes involved in light control of sexual differentiation in *Chlamydomonas reinhardtii*, 937
genetic interactions between Abelson (*Abl*) and failed axon connections (*fax*), 595
genomic location of genes controlling hypersensitive reaction to Doidge Dye in tomatoes, 675
glp-1-mediated cell signalling in *Caenorhabditis elegans*, enhancers of *glp-1*, 551
Hε46 locus in mouse, 321
hypomutable regions of *GCR1* in *Saccharomyces cerevisiae*, 1263
increased expression of *Saccharomyces cerevisiae TEF1* bypasses lethality of *TEF5* null allele, 481
interacting genes required for MC neurotransmission and pharyngeal excitation in *Caenorhabditis elegans*, 1365
interaction of ecdysone-inducible *BR-C* and *E74* genes in regulation of target gene transcription and *Drosophila* metamorphosis, 1025
LAS1 and bud morphogenesis in *Saccharomyces cerevisiae*, 857
lin-12 expression patterns during *C. elegans* hermaphrodite development, 513
mei-9 encodes a homologue of yeast excision repair protein Rad1, 619
mes-3 and germline proliferation and viability in *Caenorhabditis elegans*, 1383
molecular and mutational analysis of *flightless-I* of *Drosophila melanogaster*, 1049
molecular evolution of *Amy* locus in *Drosophila melanogaster* species subgroup, 223
molecular-marker linkage map of wheat homoeologous groups 4, 5, and 7, 721
M26 recombination hotspot activity in *Schizosaccharomyces pombe*, 33
muscle excitation genes in *Caenorhabditis elegans*, 961
mutations in *myp1* gene of *Ustilago maydis*, attenuation of mycelial growth and virulence, 491
ncl-1 as cell marker for mosaic analysis of *lin-37* and *dpy-1* in *Caenorhabditis elegans*, 989
neuronal *unc-119* gene of *Caenorhabditis elegans*, 977
nic-7, *ac-29*, and *thi-10* genes in mating type locus of *Chlamydomonas reinhardtii*, 543
Notch receptor activity and *Hairless* function during adult external sensory organ development in *Drosophila*, 1491
nucleotide polymorphism in *Esterase 6* 5'promotor region in *Drosophila melanogaster*, 215
nucleotide substitution in ribosomal RNA genes, model for estimating, 771
ovo and *otu* function in *Drosophila* oogenesis, 191
polymorphism at *Est-5B* locus in *Drosophila pseudoobscura*, 255
rec8 gene of *Schizosaccharomyces pombe*, role in linear element formation, chromosome pairing, and sister-chromatid cohesion during meiosis, 61
role of *zeste* in position-effect variegation in *Drosophila melanogaster*, 245

roles of *ABF1*, *NPL3*, and *YCL54* in silencing *Saccharomyces cerevisiae*, 889
soybean resistance genes specific for different *Pseudomonas syringae* avirulence genes, 1597
tolkin gene in *Drosophila* development, 271
white^{+} gene detection of transcriptional silencer elements in *Drosophila melanogaster*, 1075
Genetic analysis, *E. coli* periplasmic colicin V, 25
Genetic redundancy, genetic interactions between *Drosophila* Abelson (Abl) tyrosine kinase and failed axon connections (fax), 595
Genome
Drosophila melanogaster
genomic sequence of *flightless* in, 1049
S elements in, 1425
effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
genomic regions required for midgut morphogenesis of *Drosophila*, 1087
nucleotide sequence of mitochondrial genome of *Lumbricus terrestris*, 305
organization in *Caenorhabditis elegans*, 159
Genomic library, *Chlamydomonas reinhardtii*, in yeast artificial chromosomes, 87
Germline development
glp-1-mediated cell signalling in *Caenorhabditis elegans*. enhancers of *glp-1*, 551
mes-3 and germline proliferation and viability in *Caenorhabditis elegans*, 1383
selection and maintenance of sexual identity in *Drosophila* germline, 1521
Growth and development
developmental DNA rearrangements (deletion) within five species of the *Tetrahymena pyriformis* species complex, 925
effect of *sds* (suppressors of defective silencing) mutants in yeast on cell growth, 873
embryonic development in mice bearing (*7, 18*) Robertsonian translocation chromosome, 667
fs(1)Ya protein in nuclear envelope during early embryonic development of *Drosophila*, 1473
heritability of nestling growth in cross-fostered European Starlings, 657
LAS1 and bud morphogenesis in *Saccharomyces cerevisiae*, 857
maternal-effect viable mutants and morphological/behavioral defects in *Caenorhabditis elegans*, 1351
temperature-sensitive mutations affecting fin regeneration in zebrafish, 1583
Gryllus assimilis, juvenile hormone esterase, direct and correlated responses to selection, 1125

Haemonchus contortus, population genetic structure, 1007
Haemonchus placei, population genetic structure, 1007
Haplotype test, departure from neutrality in a segment of *white* gene of *Drosophila melanogaster*, 1483
Heat shock proteins, small, in plants, 785
Heitz, Emil, chloroplasts, heterochromatin, and polytene chromosomes (*Perspectives*), 7
Helianthus, introgression in, chromosomal and genetic barriers, 1163
Helicase(s), in RecF recombination pathways, 443
Heterochromatin
chloroplasts, heterochromatin, and polytene chromosomes (*Perspectives*), 7
molecular structure of centric heterochromatin in *Drosophila Dp1187* minichromosome, 283
Hitchhiking, *Drosophila melanogaster* mitochondrial DNA hitchhiking, frequency shifts of mtDNA variants and nuclear genetic background, 1113
Hotspots
decay of χ recombination hotspot activity in *Escherichia coli*, 805
HOT1 activity in *Saccharomyces cerevisiae*, 845
M26 recombination hotspot activity in *Schizosaccharomyces pombe*, 33
Hydroxyurea sensitivity, *Schizosaccharomyces pombe rad9* mutations, extragenic suppressors and, 107
Hypersensitive reaction, genomic location of genes controlling hypersensitive reaction to Doidge Dye in tomatoes, 675

Inbreeding depression
in *Agaricus bisporus*, 137
individual variation in, 1209
Intraorganismal selection, evolutionary consequences of mutation and selection within an individual, 1173
Introgression, in *Helianthus*, chromosomal and genetic barriers, 1163
Introgression lines, yield-associated QTL mapping in *Lycopersicon pennellii*, 1147
Ion channels, alternative splicing patterns and splicing signals in *Drosophila* sodium channel gene *para*, 203

Juvenile hormone esterase, in *Gryllus assimilis*, direct and correlated responses to selection, 1125

KP leucine zipper, *P* element mobility in *Drosophila melanogaster*, 587

Letter to the editor, simple regression method for interval mapping, 1657
Leucine zipper
alleles of phosphatase gene *PTC1* and of a gene encoding a putative basic leucine zipper protein, extragenic suppressors of *Saccharomyces cerevisiae pkc1* mutation and, 1275

KP leucine zipper in regulation of *P* element transposition in *Drosophila melanogaster*, 587
Lifespan, *Caenorhabditis elegans*, *age-1* and *daf-2* genes in, 1383
Light exposure, sexual differentiation in *Chlamydomonas reinhardtii*, genes involved in, 937
Linear element formation, *rec8* gene of *Schizosaccharomyces pombe* in, 61
Lumbricus terrestris, nucleotide sequence of mitochondrial genome, 305
Lycopersicon esculentum
genomic location of genes controlling hypersensitive reaction to Doidge Dye in, 675
recombination nodule map for synaptonemal complexes, 683
Lycopersicon pennellii, introgression lines for yield-associated QTL mapping, 1147

Maize
allelic interactions heritably altering activity of metastable *pl* allele, 709
functions of *En* in, 1135
recombination distances and linkage heterogeneity among maize inbreds, wide crosses, and interspecific hybrids, 1573
R-stippled
molecular organization and germinal instability, 347
paramutagenicity, 361
rust resistance, specificities associated with recombination in *Rp1 complex*, 373
teosinte branched II and evolution of maize, epistasis and dominance, 333
Mapping
advanced intercross lines, experimental population for fine mapping of QTL, 1199
chromosome maps of *Dictyostelium discoideum*, 147
comparative QTL mapping, correspondence among Poaceae QTLs affecting height and maturity, 391
genetic mapping of mating type loci in *Phytophthora infestans*, 503
genomic location of genes controlling hypersensitive reaction to Doidge Dye in tomatoes, 675
introgression line population of *Lycopersicon pennellii* for yield-associated QTL mapping, 1147
mapping of DNA polymorphisms in *Tetrahymena thermophila*, 1315
molecular-marker linkage map of wheat homoeologous groups 4, 5, and 7, 721
neuronal *unc-119* gene of *Caenorhabditis elegans*, 977
random model approach to interval mapping of QTL, 1189
recombination distances and linkage heterogeneity among maize inbreds, wide crosses, and interspecific hybrids, 1573
recombination nodule map for synaptonemal complexes of *Lycopersicon esculentum*, 683
simple regression method for interval mapping (*letter*), 1657
Suppressor-of-Tpl (SuTpl) mutation in *Drosophila melanogaster*, 1037
Mating type idiomorphs, *Neurospora* spp., species-specific and mating type-specific DNA regions adjacent to, 119
Mating type locus
Chlamydomonas reinhardtii, *nic-7*, *ac-29*, and *thi-10* genes in, 543
DNA polymorphisms in *Tetrahymena thermophila*, 1315
genetic mapping and non-mendelian segregation of mating type loci in *Phytophthora infestans*, 503
HMR locus, *sds* (suppressors of defective silencing) mutants in yeast, effects on transcriptional repression at *HMR* locus, 873
Maximum likelihood methodology
estimates of finite polygenic mixed model of inheritance, 1651
estimation of QTL parameters in half-sib design, 755
reconstruction of nucleotide or amino acid sequences of extinct ancestors, 1641
Mazamastrongylus odocoilei, population genetic structure, 1007
Median networks, mitochondrial portraits of human populations using median networks, 743
Meiosis
effect of yeast *MER* gene on chromosome synapsis and meiotic recombination, 49
heteroduplex DNA formation and homolog chromosome pairing in yeast meiotic mutants, 75
meiotic pattern of crossing over in *Caenorhabditis elegans*, *rec-1* mutant and, 1339
meiotic recombination in *Caenorhabditis elegans*, 159
M26 recombination hotspot activity in *Schizosaccharomyces pombe*, 33
rec8 gene of *Schizosaccharomyces pombe* in linear element formation, chromosome pairing, and sister-chromatid cohesion during, 61
Metamorphosis, *Drosophila*, interaction of ecdysone-inducible *BR-C* and *E74* genes in regulation of target gene transcription and metamorphosis, 1025
Methylation induced premeiotically (MIP), gene silencing, 1299
Mice
embryonic development in mice bearing (*7*, *18*) Robertsonian translocation chromosome, 667
mutations encompassing *pink-eyed dilution (p)* locus
complementation analyses, 1547
molecular analysis, 1563
transgenic insertional mutation at *Fused* locus, *Hc46* locus, 321
Mitochondrial DNA
Drosophila mtDNA hitchhiking, 1113

mitochondrial portraits of human populations using median networks, 743
population genetic structures of parasitic nematodes, 1007
sequence of mitochondrial genome of *Lumbricus terrestris*, 305
Mitotic spindle, position of mitotic spindle apparatus in *Chlamydomonas reinhardtii bld2–1* mutant lacking basal bodies, 945
Molecular probes, mutations encompassing *pink-eyed dilution (p)* locus of mouse, 1547
Mosaicism, *ncl-1* as cell marker for mosaic analysis of *lin-37* and *dpy-1* in *Caenorhabditis elegans*, 989
Muller's ratchet, epistasis and mutation effects, 431
Mutagenesis
alkylating agent-induced UV modulation of mutagenesis distinct from *E. coli* SOS and adaptive responses, 813
gypsy-P element mutagenesis in *Drosophila melanogaster*, 1061
Mutants
amber mutants of phage T4 (*Perspectives*), 439
heteroduplex DNA formation and homolog chromosome pairing in yeast meiotic mutants, 75
maternal-effect viable mutants and morphological/behavioral defects in *Caenorhabditis elegans*, 1351
molecular and mutational analysis of *flightless-I* of *Drosophila melanogaster*, 1049
position of mitotic spindle apparatus in *Chlamydomonas reinhardtii bld2–1* mutant lacking basal bodies, 945
rec-1 mutant and meiotic pattern of crossing over in *Caenorhabditis elegans*, 1339
Saccharomyces cerevisiae mutants requiring DNA topoisomerase I (*trf*), 465
sds (suppressors of defective silencing) mutants in yeast, effects on transcriptional repression at *HMR* locus, cell growth, and telomere structure, 873
vacuole defects and calcineurin in *vph6* mutants of *Saccharomyces cerevisiae*, 833
Mutation
ade6-M26, in *Schizosaccharomyces pombe*, *M26* recombination hotspot activity, 33
dominant mutations affecting muscle excitation in *Caenorhabditis elegans*, 961
dynamic. *See* Trinucleotide repeat tracts
effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
evolutionary consequences of mutation and selection within an individual, 1173
extragenic suppressors of *nudC3* mutation, 453
Δ*helD* and Δ*uvrD* mutations in RecF recombination pathway in *Escherichia coli*, 443
Muller's ratchet, epistasis and mutation effects, 431
mutations encompassing *pink-eyed dilution (p)* locus of mouse
complementation analyses, 1547
molecular analysis, 1563
myp1 gene of *Ustilago maydis*, attenuation of mycelial growth and virulence, 491
nic-7, *ac-29*, and *thi-10* auxotrophic mutations in mating type locus of *Chlamydomonas reinhardtii*, 543
nuclear migration mutations in *Aspergillus nidulans*, suppression by *tubA* alpha tubulin mutation, 1287
Saccharomyces cerevisiae pkc1 mutation, extragenic suppressors, 1275
scabrous mutations in *Drosophila melanogaster*, 607
Schizosaccharomyces pombe rad9 mutations, extragenic suppressors, radioresistance and hydroxyurea sensitivity and, 107
suppressed nonsense mutations at *elav* locus of *Drosophila*, 1101
Suppressor-of-Tpl (SuTpl) in *Drosophila melanogaster*, 1037
temperature-sensitive mutations affecting fin regeneration in zebrafish, 1583
transgenic insertional mutation at *Fused* locus, *He46* locus in mouse, 321
XO-feminizing mutations in *C. elegans*, regulatory *tra* alleles and *X* chromosome duplication, 527
Ya mutation in *Drosophila*, 1473
Mycelial growth, *Ustilago maydis*, attenuation by mutations in *myp1* gene, 491

Natural selection
evolutionary consequences of mutation and selection within an individual, 1173
Fundamental Theorem of Natural Selection in Ewens' sense, 733
heritability and selection on body size in *Drosophila buzzatii*, 181
juvenile hormone esterase in *Gryllus assimilis*, direct and correlated responses to selection, 1125
linkage disequilibria in transcriptional unit of *white* locus in natural *Drosophila melanogaster* populations, 1483
Nervous system, *Caenorhabditis elegans*, neuronal *unc-119* gene, 977
Nestling growth, heritability of nestling growth in cross-fostered European Starlings, 657
Neural development, *scabrous* mutations in *Drosophila melanogaster*, 607
Neurospora crassa, chromosome rearrangements involving nucleolus organizer region, 909
Neurospora spp., mating type idiomorphs, species-specific and mating type-specific DNA regions adjacent to, 119
Neurotransmission, MC neurotransmission and pharyn-

geal excitation in *Caenorhabditis elegans*, interacting genes required for, 1365
Neutrality, statistical tests of neutrality for DNA polymorphism data, size and power properties, 413
Neutral variants
effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
pattern of neutral molecular variation under background selection model, 1619
Nuclear envelope, fs(1)Ya protein in nuclear envelope during early embryonic development of *Drosophila*, 1473
Nuclear migration
in *Aspergillus nidulans*, extragenic suppressors of *nudC3* mutation, 453
mutations in *Aspergillus nidulans*, suppression by *tubA* alpha tubulin mutation, 1287
Nucleolus organizer region, chromosome 2, chromosome rearrangements involving, 909
Nucleotide sequence
inference method of reconstructing ancestral sequences, 1641
variation in ribosomal DNA intergenic spacer arrays of *Daphnia pulex*, 1327

Oogenesis, *Drosophila melanogaster, ovo* and *otu* function in, 191
Oomycete(s), genetic mapping and non-mendelian segregation of mating type loci in *Phytophthora infestans*, 503
Organogenesis
Drosophila Notch receptor activity and *Hairless* function during adult external sensory organ development, 1491
genomic regions required for midgut morphogenesis of *Drosophila*, 1087
Ostertagia ostertagi, population genetic structure, 1007

Paramutation/paramutagenicity
maize *pl* paramutation, 709
R-stippled maize, 361
Parasitic nematodes, population genetic structure, 1007
Parsimony method, reconstruction of nucleotide or amino acid sequences of extinct ancestors, 1641
P element
gypsy-P element mutagenesis in *Drosophila melanogaster*, 1061
mobility in *Drosophila melanogaster, KP* leucine zipper and, 587
P transposase-induced events on *P* transgene in *Drosophila*, prevalence of localized rearrangements *vs.* transpositions, 1407
Pharyngeal excitation, in *Caenorhabditis elegans*, genes required for MC neurotransmission, 1365
Phylogenetic study
evolutionary origin of nonuniversal CUG^{SER} codon in *Candida* spp., 743
mitochondrial portraits of human populations using median networks, 743
Phytophthora infestans, genetic mapping and non-mendelian segregation of mating type loci, 503
Pigmentation
allelic interactions heritably altering activity of metastable maize *pl* allele, 709
R-stippled maize
molecular organization and germinal instability, 347
paramutagenicity, 361
Plants, small heat shock proteins, 785
Poaceae, correspondence among Poaceae QTLs affecting height and maturity, 391
Polymorphism
departure from neutrality in a segment of *white* gene of *Drosophila melanogaster*, 1483
mapping of DNA polymorphisms in *Tetrahymena thermophila*, 1315
nucleotide polymorphism in *Esterase 6* 5'promotor region in *Drosophila melanogaster*, 215
polymorphism at *Est-5B* locus in *Drosophila pseudoobscura*, 255
statistical tests of neutrality, size and power properties, 413
Population genetic structure, parasitic nematodes, 1007
Position-effect variegation (PEV), *Drosophila melanogaster, zeste* in, 245
Protein kinase A, *DC2*, second *Drosophila* protein kinase A catalytic subunit gene, 1507
Pseudomonas syringae, soybean resistance genes specific for different *Pseudomonas syringae* avirulence genes, 1597

Quantitative trait loci (QTL)
advanced intercross lines, experimental population for fine mapping of QTL, 1199
correspondence among Poaceae QTLs affecting height and maturity, 391
estimation of QTL parameters in half-sib design using maximum likelihood methodology, 755
finite polygenic mixed model extended to linkage analysis, 1651
honey bee foraging behavior and, 1537
introgression line population of *Lycopersicon pennellii* for yield-associated QTL mapping, 1147
random model approach to interval mapping of QTL, 1189
simple regression method for interval mapping (*letter*), 1657
teosinte branched II and evolution of maize, epistasis and dominance, 333

Radiobiology, amber mutants of phage T4 (*Perspectives*), 439
Radioresistance, *Schizosaccharomyces pombe rad9* mutations, extragenic suppressors and, 107
Randomly amplified polymorphic DNA (RAPD) method, mapping of DNA polymorphisms in *Tetrahymena thermophila*, 1315
Reading frame, 5 S rRNA in maintenance of frame in translation, 95
Recombination
  decay of χ recombination hotspot activity in *Escherichia coli*, 805
  effects of background deleterious mutations and recombination on levels of linked neutral variation in *Drosophila* genome, 1605
  meiotic
    in *Caenorhabditis elegans*, 159
    Drosophila melanogaster mei-9 gene, 619
    effect of yeast *MER* gene, 49
    heteroduplex DNA formation and homolog chromosome pairing in yeast meiotic mutants, 75
    M26 recombination hotspot activity in *Schizosaccharomyces pombe*, 33
    rec8 gene of *Schizosaccharomyces pombe* in linear element formation, chromosome pairing, and sister-chromatid cohesion during meiosis, 61
  mitotic, *HOT1* activity in *Saccharomyces cerevisiae*, 845
  recombination between IS*200* elements and chromosomal duplications in *Salmonella typhimurium*, 1245
  recombination distances and linkage heterogeneity among maize inbreds, wide crosses, and interspecific hybrids, 1573
  in *Rp1 complex*, rust resistance in maize, 373
  two RecF recombination pathways, 443
Recombination nodules, recombination nodule map for synaptonemal complexes of *Lycopersicon esculentum*, 683
Resistance genes, soybean resistance genes specific for different *Pseudomonas syringae* avirulence genes, 1597
Rhys elements, *Escherichia coli*, 15
Ribosomal DNA, nucleotide variation in ribosomal DNA intergenic spacer arrays of *Daphnia pulex*, 1327
Ribosomal frameshifting, 5 S rRNA in maintenance of frame in translation, 95
Ribosomal RNA (rRNA)
  nucleotide substitution in, model for estimating, 771
  5 S rRNA in maintenance of frame in translation, 95
RNA polymerase I, *HOT1* activity in *Saccharomyces cerevisiae*, 845
Rp1 complex, recombination in, rust resistance in maize, 373
Rust, resistance to, specificities associated with recombination in *Rp1 complex* in maize, 373
Saccharomyces cerevisiae
  cation homeostasis, calcineurin in, 833
  effect of *MER* gene on chromosome synapsis and meiotic recombination, 49
  extragenic suppressors of *pkc1* mutation, 1275
  heteroduplex DNA formation and homolog chromosome pairing in meiotic mutants, 75
  hypomutable regions of *GCR1*, 1263
  LAS1 and bud morphogenesis in, 857
  mutants requiring DNA topoisomerase I, 465
  requirements for *HOT1* activity, 845
  silencing, roles of *ABF1*, *NPL3*, and *YCL54*, 889
  translational fidelity in elongation factor 1β deficiency suppressed by EF-1α, 481
Salmonella typhimurium, chromosomal duplications, recombination between IS*200* elements and, 1245
Schizosaccharomyces pombe
  M26 recombination hotspot activity, 33
  rad9 mutations, extragenic suppressors, radioresistance and hydroxyurea sensitivity and, 107
  rec8 gene, role in linear element formation, chromosome pairing, and sister-chromatid cohesion during meiosis, 61
Selection. *See* Natural selection
S elements, in *Drosophila melanogaster* genome, 1425
Sex determination
  autosomal component of sex determination signal of *Drosophila melanogaster*, 1451
  selection and maintenance of sexual identity in *Drosophila* germline, 1521
Sexual development, mating type idiomorphs in *Neurospora* spp., species-specific and mating type-specific DNA regions adjacent to, 119
Sexual differentiation, *Chlamydomonas reinhardtii*, genes involved in light control of, 937
Signal transduction
  alternative splicing patterns and splicing signals in *Drosophila* sodium channel gene *para*, 203
  glp-1-mediated cell signalling in *Caenorhabditis elegans*, enhancers of *glp-1*, 551
  scabrous mutations in *Drosophila melanogaster*, 607
  sex determination in *Drosophila* germline, 1521
"Silencer trap", *white*$^+$ gene detection of transcriptional silencer elements in *Drosophila melanogaster*, 1075
Silencing
  gene silencing by methylation induced premeiotically (MIP) in *Ascobolus immersus*, 1299
  in *Saccharomyces cerevisiae*, roles of *ABF1*, *NPL3*, and *YCL54*, 889
  sds (suppressors of defective silencing) mutants in yeast, effects on transcriptional repression at *HMR* locus, cell growth, and telomere structure, 873
Skeletal muscle, muscle excitation genes in *Caenorhabditis elegans*, 961

Sodium channel, alternative splicing patterns and splicing signals in *Drosophila* sodium channel gene *para*, 203
Splicing, alternative splicing patterns and splicing signals in *Drosophila* sodium channel gene *para*, 203
Statistical tests
analysis of conditional genetic effects and conditional variance components, 1633
neutrality for DNA polymorphism data, size and power properties, 413
Sturnus vulgaris, heritability of nestling growth in cross-fostered European Starlings, 657
Sturtevant, Alfred Henry (*Perspectives*), 1227
Synaptonemal complexes
effect of yeast *MER* gene on chromosome synapsis and meiotic recombination, 49
recombination nodule map for synaptonemal complexes of *Lycopersicon esculentum*, 683

Teladorsagia circumcincta, population genetic structure, 1007
Telomeres, effect of *sds* (suppressors of defective silencing) mutants in yeast on telomere structure, 873
Temperature stress, small heat shock proteins in plants, 785
Tetrahymena pyriformis species complex, developmental DNA rearrangements (deletion) within five species, 925
Tetrahymena thermophila, mapping DNA polymorphisms closely linked to mating type locus, 1315
tolloid/BMP-1 family, *tolkin* gene in *Drosophila* development, 271
Tomato. *See Lycopersicon esculentum*
Topoisomerase I, *Saccharomyces cerevisiae* mutants requiring DNA topoisomerase I (*trf*), 465
Transcription
interaction of ecdysone-inducible *BR-C* and *E74* genes in regulation of target gene transcription and *Drosophila* metamorphosis, 1025
role of *zeste* in *Drosophila melanogaster*, 245
Saccharomyces cerevisiae mutants requiring DNA topoisomerase I (*trf*), 465
sds (suppressors of defective silencing) mutants in yeast, effects on transcriptional repression at *HMR* locus, cell growth, and telomere structure, 873
Transformation, *Bacillus subtilis*, size and continuity of DNA segments integrated in, 1231
Translation
elongation factor 1β deficiency suppressed by EF-1α in *Saccharomyces cerevisiae*, 481
5 S rRNA in maintenance of frame in, 95
Transposable elements. *See also P* element
functions of *En* in maize, 1135
S elements in *Drosophila melanogaster* genome, 1425
unlinked transposed dissociation elements in tomato, 383
Transposition
KP leucine zipper in regulation of *P* element transposition in *Drosophila melanogaster*, 587
P transposase-induced events on *P* transgene in *Drosophila*, prevalence of localized rearrangements *vs.* transpositions, 1407
unlinked transposed dissociation elements in tomato, 383
Transvection, role of *zeste* in *Drosophila melanogaster*, 245
Trinucleotide repeat tracts, folding into hairpin secondary structure, 825

Unigenic evolution, putative leucine zipper that mediates dimerization of *Saccharomyces cerevisiae* Gcr1p, 1263
Ustilago maydis, mutations in *myp1* gene, attenuation of mycelial growth and virulence, 491
UVM (UV modulation of mutagenesis), alkylating agent-induced, in *E. coli*, 813

Virulence, *Ustilago maydis*, attenuation by mutations in *myp1* gene, 491

Wheat, molecular-marker linkage map of wheat homoeologous groups 4, 5, and 7, 721
Wolbachia variants, variability within Seychelles cytoplasmic incompatibility system in *Drosophila simulans*, 1015

Xanthomonas campestris pv. *vesicatoria* (Doidge) Dye, genomic location of genes controlling hypersensitive reaction to Doidge Dye in tomatoes, 675
X chromosome
effect of *X*:A chromosome balance on sex determination in *Drosophila melanogaster*, 1451
XO-feminizing mutations in *C. elegans*, *eDp26* duplication, 527

Yeast. *See also specific yeasts*
construction of *Chlamydomonas reinhardtii* genomic library in yeast artificial chromosomes, 87
RAP1 overexpression, molecular and genetic analysis of toxic effect, 1253
sds (suppressors of defective silencing) mutants, effects on transcriptional repression at *HMR* locus, cell growth, and telomere structure, 873